

WHAT IS CLAIMED:

1. A chimeric gene comprising:
 - a first DNA molecule encoding a hypersensitive response elicitor protein or polypeptide,
 - a promoter operably linked 5' to the first DNA molecule to induce transcription of the first DNA molecule in response to activation of the promoter by an oomycete, and
 - a 3' regulatory region operably linked to the first DNA molecule.
2. The chimeric gene according to claim 1 further comprising:
 - a second DNA molecule encoding a secretion signal polypeptide, the second DNA molecule being operably linked between the promoter and the first DNA molecule.
3. The chimeric gene according to claim 2, wherein the second DNA molecule encodes a secretion signal polypeptide comprising an amino acid sequence of SEQ. ID. No. 11, SEQ. ID. No. 13, SEQ. ID. No. 15, or SEQ. ID. No. 17.
4. The chimeric gene according to claim 3, wherein the second DNA molecule comprises a nucleotide sequence of nt 8-110 from SEQ. ID. No. 10, SEQ. ID. No. 12, SEQ. ID. No. 14, or SEQ. ID. No. 16.
5. The chimeric gene according to claim 1, wherein the promoter is a *gst1* promoter.
6. The chimeric gene according to claim 1, wherein the *gst1* promoter comprises a nucleotide sequence of SEQ. ID. No. 9 or effective fragments thereof.
7. The chimeric gene according to claim 1, wherein the hypersensitive response elicitor protein or polypeptide is derived from a species of pathogen selected from the group consisting of *Erwinia*, *Xanthomonas*, *Pseudomonas*, *Phytophthora*, and *Clavibacter*.

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8. The chimeric gene according to claim 7, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Erwinia amylovora*.

9. The chimeric gene according to claim 8, wherein the first DNA molecule encodes a hypersensitive response elicitor protein or polypeptide comprising an amino acid sequence of SEQ. ID. No. 3.

10. The chimeric gene according to claim 9, wherein the first DNA molecule comprises a nucleotide sequence of SEQ. ID. No. 4.

11. The chimeric gene according to claim 7, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Erwinia carotovora*.

12. The chimeric gene according to claim 7, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Erwinia stewartii*.

13. The chimeric gene according to claim 7, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Erwinia chrysanthemi*.

14. The chimeric gene according to claim 13, wherein the first DNA molecule encodes a hypersensitive response elicitor protein or polypeptide comprising an amino acid sequence of SEQ. ID. No. 1.

15. The chimeric gene according to claim 14, wherein the first DNA molecule comprises a nucleotide sequence of SEQ. ID. No. 2.

16. The chimeric gene according to claim 7, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Pseudomonas syringae*.

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17. The chimeric gene according to claim 16, wherein the first DNA molecule encodes a hypersensitive response elicitor protein or polypeptide comprising an amino acid sequence of SEQ. ID. No. 5.

18. The chimeric gene according to claim 17, wherein the first DNA molecule comprises a nucleotide sequence of SEQ. ID. No. 6.

19. The chimeric gene according to claim 7, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Pseudomonas solanacearum*.

20. The chimeric gene according to claim 19, wherein the first DNA molecule encodes a hypersensitive response elicitor protein or polypeptide comprising an amino acid sequence of SEQ. ID. No. 7.

21. The chimeric gene according to claim 20, wherein the first DNA molecule comprises a nucleotide sequence of SEQ. ID. No. 8.

22. An expression system comprising a vector into which is inserted a chimeric gene according to claim 1.

23. A host cell comprising a chimeric gene according to claim 1.

24. The host cell according to claim 23, wherein the host cell is a bacterial cell or a plant cell.

25. The host cell according to claim 24, wherein the bacterial cell is an *Agrobacterium* cell.

26. The host cell according to claim 24, wherein the host cell is a plant cell.

27. The host cell according to claim 26, wherein the hypersensitive response elicitor protein or polypeptide is derived from a species of pathogen selected from the group consisting of *Erwinia*, *Xanthomonas*, *Pseudomonas*, *Phytophthora*, and *Clavibacter*.

28. The host cell according to claim 26, wherein the chimeric gene further comprises

a second DNA molecule encoding a secretion signal polypeptide, the second DNA molecule being operably linked between the promoter and the first DNA molecule.

29. The host cell according to claim 26, wherein the promoter is a *gst1* promoter.

30. A transgenic plant resistant to disease resulting from oomycete infection, the transgenic plant comprising:

a chimeric gene according to claim 1, wherein the promoter induces transcription of the first DNA molecule in response to infection of the plant by an oomycete.

31. The transgenic plant according to claim 30, wherein the chimeric gene further comprises

a second DNA molecule encoding a secretion signal, the second DNA molecule being operably linked between the promoter and the first DNA molecule.

32. The transgenic plant according to claim 31, wherein the second DNA molecule encodes a secretion signal polypeptide comprising an amino acid sequence of SEQ. ID. No. 11, SEQ. ID. No. 13, SEQ. ID. No. 15, or SEQ. ID. No. 17.

33. The transgenic plant according to claim 32, wherein the second DNA molecule comprises a nucleotide sequence of nt 8-110 from SEQ. ID. No. 10, SEQ. ID. No. 12, SEQ. ID. No. 14, or SEQ. ID. No. 16.

34. The transgenic plant according to claim 30, wherein the *gst1* promoter comprises a nucleotide sequence of SEQ. ID. No. 9 or effective fragments thereof.

35. The transgenic plant according to claim 30, wherein the oomycete is a species of *Plasmopara*, *Phytophthora*, *Peronospora*, *Pseudoperonospora*, *Bremia*, *Sclerospora*, *Aphanomyces*, *Pythium*, or *Albugo*.

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36. The transgenic plant according to claim 30, wherein the transgenic plant is selected from a group consisting of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

37. The transgenic plant according to claim 36, wherein the transgenic plant is a grape plant.

38. The transgenic plant according to claim 37, wherein the oomycete is selected from the group consisting of *Plasmopara viticola* and *Phytophthora parasitica*.

39. The transgenic plant according to claim 36, wherein the transgenic plant is a tobacco plant.

40. The transgenic plant according to claim 39, wherein the oomycete is selected from the group consisting of *Peronospora tabacina*, *Pythium* spp., and *Phytophthora* spp.

41. The transgenic plant according to claim 30, wherein the hypersensitive response elicitor protein or polypeptide is derived from a species of pathogen selected from the group consisting of *Erwinia*, *Xanthomonas*, *Pseudomonas*, *Phytophthora*, and *Clavibacter*.

42. The transgenic plant according to claim 41, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Erwinia amylovora*.

43. The transgenic plant according to claim 42, wherein the first DNA molecule encodes a hypersensitive response elicitor protein or polypeptide comprising an amino acid sequence of SEQ. ID. No. 3.

44. The transgenic plant according to claim 44, wherein the first DNA molecule comprises a nucleotide sequence of SEQ. ID. No. 4.

45. The transgenic plant according to claim 41, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Erwinia carotovora*.

46. The transgenic plant according to claim 41, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Erwinia stewartii*.

47. The transgenic plant according to claim 41, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Erwinia chrysanthemi*.

48. The transgenic plant according to claim 47, wherein the first DNA molecule encodes a hypersensitive response elicitor protein or polypeptide comprising an amino acid sequence of SEQ. ID. No. 1.

49. The transgenic plant according to claim 48, wherein the first DNA molecule comprises a nucleotide sequence of SEQ. ID. No. 2.

50. The transgenic plant according to claim 41, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Pseudomonas syringae*.

51. The transgenic plant according to claim 50, wherein the first DNA molecule encodes a hypersensitive response elicitor protein or polypeptide comprising an amino acid sequence of SEQ. ID. No. 5.

52. The transgenic plant according to claim 51, wherein the first DNA molecule comprises a nucleotide sequence of SEQ. ID. No. 6.

53. The transgenic plant according to claim 41, wherein the hypersensitive response elicitor protein or polypeptide is derived from *Pseudomonas solanacearum*.

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54. The transgenic plant according to claim 53, wherein the first DNA molecule encodes a hypersensitive response elicitor protein or polypeptide comprising an amino acid sequence of SEQ. ID. No. 7.

55. The transgenic plant according to claim 54, wherein the first DNA molecule comprises a nucleotide sequence of SEQ. ID. No. 8.

56. The transgenic plant according to claim 30, wherein the chimeric gene is stably inserted into the genome of the transgenic plant.

57. A method of making a recombinant plant cell comprising:
transforming a plant cell with a chimeric gene according to claim 1
under conditions effective to yield transcription of the first DNA molecule in response
to oomycete-induced activation of the promoter.

58. A method of making a plant resistant to disease resulting from
oomycete infection, the method comprising:

transforming a plant cell with a chimeric gene according to claim 1
under conditions effective to yield transcription of the first DNA molecule in response
to oomycete-induced activation of the promoter and
regenerating a plant from the transformed plant cell.

59. The method according to claim 58, wherein said transforming
is performed under conditions effective to insert the chimeric gene into the genome of
the plant cell.

60. The method according to claim 58, wherein said transforming
is *Agrobacterium* mediated.

61. The method according to claim 58, wherein said transforming
comprises:

propelling particles at the plant cell under conditions effective for the
particles to penetrate into the cell interior and

introducing an expression vector comprising the chimeric gene into the
plant cell interior.

62. The method according to claim 58, wherein the chimeric gene further comprises

a second DNA molecule encoding a secretion signal, the second DNA molecule being operably linked between the promoter and the first DNA molecule.

63. The method according to claim 58, wherein the promoter is a *gst1* promoter.

64. The method according to claim 58, wherein the oomycete is a species of *Plasmopara*, *Phytophthora*, *Peronospora*, *Pseudoperonospora*, *Bremia*, *Sclerospora*, *Aphanomyces*, *Pythium*, or *Albugo*.

65. The method according to claim 58, wherein the transgenic plant is selected from the group consisting of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

66. The method according to claim 65, wherein the transgenic plant is a grape plant.

67. The method according to claim 66, wherein the oomycete is selected from the group consisting of *Plasmopara viticola* and *Phytophthora parasitica*.

68. The method according to claim 65, wherein the transgenic plant is a tobacco plant.

69. The method according to claim 68, wherein the oomycete is selected from the group consisting of *Peronospora tabacina*, *Phytophthora* spp., and *Pythium* spp.

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70. The method according to claim 58, wherein the hypersensitive response elicitor protein or polypeptide derives from a species of pathogen selected from the group consisting of *Erwinia*, *Xanthomonas*, *Pseudomonas*, *Phytophthora*, and *Clavibacter*.

71. A transgenic plant seed obtained from the transgenic plant according to claim 30.

72. A transgenic plant scion or rootstock cultivar obtained from the transgenic plant according to claim 30.